

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 00:44:04 ; Search time 691 Seconds

(without alignments)
1190.223 Million cell updates/sec

Title: US-09-515-806A-1

Perfect score: 5525

Sequence: 1 tcggcccacgcgtcgacc.....aatgctttcatataccgtca 5525

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 870388 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

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Qy	357	TCAAATGAAAGTGTCAATTGTGTTAAATCTGCCDPAAGAGAAACTGGCAGGAAACACTGT	416	Qy	1427	GGAGGATGTGTTGAGCAAAACCCGAGTTGGTTTAASTGACAAATGCTCTGCCCTATAAAAC	1486
Db	301	TCAAATGAAAGTGTCAATTGTGTTAAATCTGCCDPAAGAGAAACTGGCAGGAAACACTGT	360	Db	1380	GGAGGATGTGTTGAGCAAAACCCGAGTTGGTTTAASTGACAAATGCTCTGCCCTATAAAAC	1439
Qy	417	GGGGAG---GTTATGATCTTGTGACTCTGCTTACACGTGAGTCATTCTAGCGAGAT	473	Qy	1487	GGGAGAGAAAGGAGATGTTGGCCTTCTGCTGTCAGCCAAAGGACA	1546
Db	361	GGGGAGGTAGTGTGATCTGTTGACTCTGCTTACACGTGAGTCATTCTAGCGAGCT	420	Db	1440	GGGGAGAGAAAGGAGATGTTGGCCTTCTGCTGTCAGCCAAAGGACA	1499
Qy	474	AACAGGCCCTCCAAAGTCCTTCACTGAAAGAATCTGTTAAAGGGGGTCAGGGAG	533	Qy	1547	GGATGTTGAGAGTACCTGTGACCATCCPAGTGTGACTTACAGTGACCTTCAGGTT	1606
Db	421	AACAGGCCCTCCAAAGTCCTTCACTGAAAGAACTGGCAGGAAACACTGT	360	Db	1500	GGATGTTGAGAGTACCTGTGACCATCCPAGTGTGACTTACAGTGACCTTCAGGTT	1559
Qy	534	CAGCAGGGCTTGGAGGCCAAAGGCAAGGCAAGTGAATCTGCT	593	Qy	1607	TCTAAAGAA---ATGTTGTTGCTGATGACAAAGAAATGGTGTGCTCCAGCTGTT	1663
Db	481	CAACAGAGGCTTGGCCAAAGGCAAGGCAAGTGAATCTGCT	540	Db	1560	TCTAAAGAAAGGAGATGTTGCTGATGACAAAGAAATGGTGTGCTCCAGCTGTT	1619
Qy	594	GAGATTGAGAGGAAAGAGAACTAAAGAGAAATGCTG	653	Qy	1664	GAACACAGCCTTATAAATCCCGAGGAAAATGCCCTCTAGTGGAAACAAAGTCCTGAAGA	1723
Db	541	GAGATTGAGAGGAAAGAGAACTAAAGAGAAATGCTG	600	Db	1620	GAACACAGCCTTATAAATCCCGAGGAAAATGCCCTCTAGTGGAAACAAAGTCCTGAAGA	1677
Qy	654	CAGAAACCTTTGAAATTGCTAGTGTCAACCCCTAAGAAGGACCA	713	Qy	1784	CTTCCTTAGTGGACACAGAGACAGTTCCGATACTTCTGGATACTTCTGGTTGAGAAATTACA	1843
Db	601	CAGAACCTTGGAAATTGCTAGTGTCAACCCCTAAGAAGGACCA	660	Db	1737	CTTCCTTAGTGGACACAGAGACAGTTCCGATACTTCTGGTTGAGAAATTACA	1796
Qy	714	GGGGACACAGAACGGTGTGCACTTGTGACATCTGCT	773	Qy	1783	CTTCCTTAGTGGACACAGAGACAGTTCCGATACTTCTGGTTGAGAAATTACA	1783
Db	661	GGGGACACAGAACGGTGTGCACTTGTGACATCTGCT	720	Db	1678	-CTCTGAGGACAGATGTTGAGCTGTTCTGAGCTTACCCAGTGTGCT	1736
Qy	774	AAACATGGCRAACTCTCAGGAAGSTCT---AGGGAGACGTCACTTGTG	827	Qy	1844	ACTCTTGTGAAAGGAGCTTGGGCTCATCAAGTGTGACATGTTGAGCTGACCGCTG	1903
Db	721	AAACATGGCRAACTCTCAGGAAGSTCTTGTGACATCTGCT	780	Db	1797	ACTCTTGTGAAAGGAGCTTGGGCTCATCAAGTGTGACATGTTGAGCTGACCGCTG	1856
Qy	828	TGTAATAGTGGAGATCTCTGGCTTGTGAAATTCTGTGTTAAATGGGAGTCCT	887	Qy	1904	CTCTACCGCTGACGGCATCCATCAACCCGGCAGTCCTGGGCTACTACAGGC	1963
Db	781	TGTAATAGTGGAGATCTCTGGCTTGTGAAATTCTGTGTTAAATGGGAGTCCT	840	Db	1857	CTCTACCGCTGACGGCATCCATCAACCCGGCAGTCCTGGGCTACTACAGGC	1916
Qy	888	GATCAGCTCATGGTCAAAAGGAATGTTGGCAAGTGTGAACTTGGAAATTAA	947	Qy	1964	GGGGAAAGTGACACTGTGTCAGGTGCACTGGTGTGACATGGGCTACTCCGGCC	2023
Db	841	GATCAGCTCATGGTCAAAAGGAATGTTGGCAACTTGGAAATTAA	900	Db	1917	GGGGAAAGTGACACTGTGTCAGGTGCACTGGTGTGACATGGGCTACTCCGGCC	1976
Qy	948	GCTCTACAAATGCTTGGAAACGCCACTGGTGGCTTGTGTTGATGTTGGGTCCCT	1007	Qy	2024	CTGGATGCAAGGCGCACAGGCCGGGACGGCCGGGACTCCGGCC	2083
Db	901	GTCATACATGGAAACGCCACTGGTGGCTTGTGTTGATGTTGGGTCCCT	960	Db	1977	CTGGATGCAAGGCGCACAGGCCGGGACTCCGGCC	2036
Qy	1008	CAGTGGCAAAAGGAACTGGTCACTCTTACCACTGAGAAAGAGATGATAG	1067	Qy	2084	CTCTGGCAAGGATGACCGAGCTGGCAGCGGGGAGACAGAGCGGCTGGGA	2143
Db	961	CAGTGGCAAAAGGAACTGGTCACTCTTACCACTGAGAAAGAGATGATAG	1020	Db	2037	CTCTGGCAAGGATGACCGAGCTGGCAGCGGGGAGACAGAGCGGCTGGGA	2096
Qy	1068	TGAAAAGAGCAGATTCAGGAAAGAACTGAACTCTGCAATGAAATTGGGCT	1127	Qy	2114	CACCGTAGGGCCGCGGCCACCCATCTCAGAGCTGGTGGAGCTGGACCTTC	2203
Db	1021	TGCAAAAGAGCAGATTCAGGAAAGAACTGAACTCTGCAATGAAATTGGGCT	1080	Db	2097	CACCGTAGGGCCGCGGCCACCCATCTCAGAGCTGGTGGAGCTGGACCTTC	2156
Qy	1128	CCAAATGCTGAGCTACCTGCAATGAACTCTGCAACCTGGCCACTCAGC	1186	Qy	2204	GGCGAGGGCTGGCAGTCAGTCGGCTTCTGGCTTCCTGGCTTCCTGGCT	2263
Db	1081	CCAAATGCTGAGCTACCTGCAATGAACTCTGCAACCTGGCCACTCAGC	1139	Db	2157	GGCGAGGGCTGGCAGTCAGTCGGCTTCTGGCTTCCTGGCTTCCTGGCT	2216
Qy	1187	GGACATTTAGTGGAGCACTTGGTCACTTGGCACTCTGGCTTCCTGGCT	1246	Qy	2264	GGACGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2323
Db	1140	GGACATTTAGTGGAGCACTTGGTCACTTGGCTTCCTGGCTTCCTGGCT	1199	Db	2227	GGACGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2276
Qy	1247	CCCCATCCCTGTGCACTAGCTGGTCACTAGCTGGTCACTAGCTGGCT	1259	Qy	2324	TCTGAAAGTGTGATATCTCTGACATGAGATGAACTGAAAGTCAAGATGGAA	2383
Db	1200	CCCCATCCCTGTGCACTAGCTGGTCACTAGCTGGTCACTAGCTGGCT	1259	Db	2277	TCTGAAAGTGTGATATCTCTGACATGAGATGAACTGAAAGTCAAGATGGAA	2336
Qy	2384	TGAGGATTGCAATGAAAGAATGGCTCCATGAAAGTGAAGTCAAGTGGCT	2443	Qy	2384	TGAGGATTGCAATGAAAGAATGGCTCCATGAAAGTGAAGTCAAGTGGCT	2443

Db	2337	TGAGATTGCAATGAAAATGGCTCCATGAAACTGACCCATAGTGCGACTGGCC	2396	Db	3417	AAACGGTACTGCATAGAACGTTGTTACCCGCCAAGTTAGATGATGTTCACTCCAA	3476
Qy	2444	TGTGCACTACCPATACTCATCAGATGGACTCTGTGAGAAAGGACTTTAGAGACACAT	2503	Qy	3524	AGBACTCTGGGGAGTGCATTGATATTGATCTACCTTACCTACAGCTTTCGCCCCAC	3583
Db	2397	TGTGCACTACCPATACTCATCAGATGGACTCTGTGAGAAAGCACCAT	2456	Db	3447	AGACATCTGGGGAGTGCATTGATATTGATCTACCTTACCTACAGCTTTCGCCCCAC	3536
Qy	2504	TGACCGGGACTGTATCGAGAACCGCTCAGACTCTGGGTTTTCGAGAGATTCTGAA	2563	Qy	3584	TGTTGAATTATCTACTAATCTAATGATCCAGAGTTCCAGACTTCAGGAAG	3643
Db	2457	TGACCGGGACTGTATCGAGAACCGCTCAGACTCTGGGTTTTCGAGAGATTCTGAA	2516	Db	3537	TGTTGAATTATCTACTAATCTAATGATCCAGAGTTCCAGACTTCAGGAAG	3596
Qy	2564	TGGATTACCTATATCCATGAGAAAGGATTGATTACACCGGATTGAAACCTGAA	2623	Qy	3644	AAATTACAGTATTATTGAAACCATACATGAACTTATGAAAGCAATTCTGTTGG	3703
Db	2517	TGGATTACCTATATCCATGAGAAAGGATTGATTACCCGATTGAAACCTGAA	2576	Db	3597	AAATTACAGTATTATTGAAACCATACATGAACTTATGAAAGCAATTCTGTTGG	3656
Qy	2624	TTTTTGATTTCTGATGACATGTGAAATAAGGTGATTGCTGGCAGGCACT	2683	Qy	3704	GATCCCCAGAAGATAAACTCAGTCACCTACATTATCTGTGACAGAGAA	3763
Db	2577	TTTTTGATTTCTGATGACATGTGAAATAAGGTGATTGCTGGCAGGCACT	2636	Db	3657	GATCCCCAGAAGATAAACTCAGTCACCTACATTATCTGTGACAGAGAA	3716
Qy	2684	AGCCTTTCTGCTGACGACAAACAGACGATCAGACAGACTGATGAGACCC	2743	Qy	3764	GCTGACCGAGGAGAGAACTGGGAAGCTAAATTGTAATCTGCTTGTCTCTAA	3823
Db	2637	AGCCTTTCTGCTGACGACAAACAGACGATCAGACAGACTGATGAGACCC	2696	Db	3717	GCTGACCGAGGAGAGAACTGGGAGCTTAATTTGTAATCTGCTTGTCTCTAA	3776
Qy	2744	TTCAGGTCACCTAACTGGGATGGTGGCATGCTCTCATGTAAGCCAGAGTCCAAG	2803	Qy	3824	GRTGCACTCTACAAGTATTGACAGAACGTTATTGACAGTGTGGGAACATATGGCTTAAAGAA	3883
Db	2697	TTCAGGTCACCTAACTGGGATGGTGGCATGCTCTCATGTAAGCCAGAGTCCAAG	2756	Db	3837	AAATTCAATAATGAAAGAAACGTTATTGACAGTGTGGCTTAAAGAA	3896
Qy	2804	AAGCACCAATCTGCTACAAACCAAGAAGTGTCTCTGGGATTCTCTT	2863	Db	3777	GRTGCACTCTACAAGTATTGACAGAACGGGATTTGAAAGTCTCTCAAA	3836
Db	2757	AAGCACCAATCTGCTACAAACCAAGAAGTGTCTCTGGGATTCTCTT	2816	Qy	3884	AAATTCAATAATGAAAGAAACGTTATTGACAGTGTGGGAACATATGGCTTAAAGAA	3943
Qy	2864	TGAGATGTCCTATCACCCCATGTCAGGGTCAAGAAGGATCTTGTCTCAACCACT	2923	Qy	3897	CTTAAACGAGGGAAAGGGGTGTACTTGAAGAAACTCAGCTTAACTGCTTAA	3956
Db	2817	TGAGATGTCCTATCACCCCATGTCAGGGTCAAGAAGGATCTTGTCTCAACCACT	2876	Db	3998	GATCAAATTGGCTTACAGGTGACAGGCAATTGAACTCTTCAGCTTGT	4057
Qy	2924	CAGAGATCCACTTGCCTAACTTCCAGAAGACTTGCACATGGAGGATGCAAAGCA	2983	Qy	4057	GGTATCATCAACGAGGAAAGGGGTGTACCTGTAATCTGAAATCTGCAAGTGT	4057
Db	2937	GAATATCACTCATCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGG	3016	Db	3957	GATCAAATTGGCTTACAGAGGAAACCTGCAATTCTTCAGCTTGT	4016
Qy	2864	TGAGATGTCCTATCACCCCATGTCAGGGTCAAGAAGGATCTTGTCTCAACCACT	2923	Qy	3944	CTTAAACGAGGGCTGACTCTGGCTACTTGAAGAAACTCAGCTTAACTGCTTAA	3997
Db	2887	TGAGATGTCCTATCACCCCATGTCAGGGTCAAGAAGGATCTTGTCTCAACCACT	2983	Db	3897	CTTAAACGAGGGAAAGGGGTGTACTTGAAGAAACTCAGCTTAACTGCTTAA	3956
Qy	2984	GAATTCAGTCATCTCCCTGGCTGTAACCCAGATGCAATTGCTGGCTCAACCACT	3043	Qy	4058	GGTTTTCATCAAACGAGGAAAGGGGTGTACCTGTAATCTGAAATCTGCAAGTGT	4117
Db	2937	GAATATCACTCATCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGG	2996	Db	4017	GGTATCATCAACGAGGAAAGGGGTGTACCTGTAATCTGAAATCTGCAAGTGT	4076
Qy	2877	CAGAGATCCACTTGCCTAACTTCCAGTAAAGGATCTTCAAGAAGGATGCAAAGCA	2936	Qy	4118	TGACCTGTGTGATCTCCAGTTAGGGCCAGTGGCTGAGGAGATA	4177
Db	2817	TGAGATGTCCTATCACCCCATGTCAGGGTCAAGAAGGATCTTGTCTCAACCACT	2876	Db	4077	TGACCTGTGTGATCTCCAGTTAGGGCCAGTGGCTGAGGAGATA	4136
Qy	2924	CAGAGATCCACTTGCCTAACTTCCAGAAGACTTGCACATGGAGGATGCAAAGCA	2983	Qy	4178	TGGGGTCACTAGCTTAACTGAACTATGCAAGATATGCTGCTCTCAACATGGAGAA	4232
Db	2937	GAATATCACTCATCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGG	3016	Db	4137	TGGGGTCACTAGCTTCACTGAACTATGCAAGATATGCTGCTCTCAACATGGAGAATCTG	4196
Qy	2864	ACTGCTCAAGATGTCAGTGTCTGCCCATCCAGATGGAGGATGAGGTCACTGAACT	3103	Qy	4233	---TCGTTACATAATAGACTCTGGCTCTGGGTAACTGTTGAGTGTGCAATGTC	4288
Db	2937	ACTGCTCAAGATGTCAGTGTCTGCCCATCCAGATGGAGGATGAGGTCACTGAACT	3056	Qy	4197	AAGTTCTGTTACAACTGCTCTGGGBCCTCTGGTTAACTGTTGAGTGTGCAATGTC	4256
Qy	3104	GCTGCACTAACCCCTGACCAACGGTGTGGAGGGCTACCGCAGATGGCTGCCAGAT	3163	Db	4289	GTCCAGGGCCATCAACCTAACCTAACCTAACCTAACCTAACCTAACCTAACCTAAC	4348
Db	3057	GCTGCACTAACCCCTGACCAACGGCAGATGGCTACCGCAGATGGCTGCCAGAT	3116	Qy	4257	GTCCAGGGCCATAAACCTAACCTAACCTAACCTAACCTAACCTAACCTAACCTAAC	4316
Qy	3164	CCTCTCGCAAGCCTGCCATCGATTACACCTTACAGGAACTGAGCTGAGGAGG	3223	Db	4349	GTACGACTGGCTAATGCTGGCCCTTGTCTGGATTAAGGAAAGCTTAACTG	4402
Db	3117	CCTCTCGCAAGCCTGCCATCGATTACACCTTACAGGAACTGAGCTGAGGAGG	3176	Qy	4337	AATCACCTATGIGGGCCCTTGTCTGGATTAAGGAAAGCTTAACTG	4436
Qy	3224	CAACTTCCTCAATCGTACAGCCAAAGATGCCAGCATGTCAGTGTGAAACCATCATCGCAT	3283	Db	4463	CAGAAAGGAAAGCCATGTCAGTGTGAACTGTCAGTGTGAACTGTCAGTGT	4522
Db	3177	CAACTTCCTCAATCGTACAGCCAAAGATGCCAGCATGTCAGTGTGAAACCATCATCGCAT	3236	Qy	4317	GTACGACTGGCTAATGCTGGCCCTTGTCTGGATTAAGGAAAGCTTAACTG	4376
Qy	3284	CITTAAGAACACATGGAGTGTGTCATTGTCACCTACTGTCAGTGTGAAACAGACA	3343	Db	4437	CAGAAAGGAAAGCCATGTCAGTGTGAACTGTCAGTGTGAACTGTCAGTGT	4496
Db	3237	CITTAAGAACACATGGTCATGTCAGTGTGAACTGTCAGTGTGAAACAGACA	3296	Qy	4403	AATCACCTATGIGGGCCCTTGTCTGGATTAAGGAAAGCTTAACTG	4462
Qy	3344	AATAATGAGCAACGGCTGCCCTATCATGGACCAAGGCTGAGCTGAGCTGAGGAA	3403	Db	4377	AATCACCTATGIGGGCCCTTGTCTGGATTAAGGAAAGCTTAACTG	4436
Db	3297	AATAATGAGCAACGGCTGCCCTATCATGGACCAAGGCTGAGCTGAGCTGAGGAA	3356	Qy	4404	TCCCTTGCACCTGGGATCCCTTGTGAAAGATACTGTCAGTGTGAACTGTCAGTGT	4582
Qy	3404	TCCCTTGCACCTGGGATCCCTTGTGAAAGATACTGTCAGTGTGAACTGTCAGTGT	3463	Db	3357	TCCCTTGCACCTGGGATCCCTTGTGAAAGATACTGTCAGTGTGAACTGTCAGTGT	3523
Db	3357	TCCCTTGCACCTGGGATCCCTTGTGAAAGATACTGTCAGTGTGAACTGTCAGTGT	3416	Qy	4497	GCAGAAACTGAGGACTAAAGTCACGTGTTGTCAGGCCAGTGTGAACTGTCAGTGT	4556

Qy	4583	TGCACTGCAAATCTGAGGGTCATTTCTAAATGTTAGGTTGTTGAAATCCATGG	4642	Qy	2605	ATTTGAAAGCCCTGTCACATTTGGATTCTGATGACCATGTTGAAAAATAGGTGATTGG	2664
Db	4557	TGCACTGCAAATCTGAGGGTCATTTCTAAATGTTAGGTTGTTGAAATCCATGG	4616	Db	132	ATTTGAAAGCCCTGTCACATTTGGATTCTGATGACCATGTTGAAAAATAGGTGATTGG	191
Qy	4643	ACCAACATGGTTCCATGTTGAGTGTGCTAGGCCCGAGAGCTGAGCCAGCACTAG	4702	Qy	2665	GTGTTGGGACACAGACCACTAGGCTTCTGCTGACGCCAAACAGGATCAGACGGAG	2724
Db	4617	ACCAACATGGTTCCATGTTGAGTGTGCTAGGCCCGAGAGCTGAGCCAGCACTAG	4676	Db	192	GTGTTGGGACACAGACCACTAGGCTTCTGCTGACGCCAAACAGGATCAGACGGAG	251
Qy	4703	GAGGGCTATGAAACTCAGGTACACTTGAGCAACTTGTGAGCTTGTGAGCTTGT	4762	Qy	2725	ACTTGATTAACTGACCCCTAGGTACTAACTGGATGTTGGACTGCTCTATG	2784
Db	4677	GAGGGCTATGAAACTCAGGTACACTTGAGCAACTTGTGAGCTTGTGAGCTTGT	4736	Db	252	ACTTGATTAACTGACCCCTAGGTACTAACTGGATGTTGGACTGCTCTATG	311
Qy	4763	GAAAAGCAGTGAATTGAAATTCTGGCT--GTGAGTCACTCCAGAAACAAATTAC	4819	Qy	2785	TAAGCCAGAGGTCCAGGAACCAATCTGATACAAACAGAAAGTGGATCTCTTCA	2844
Db	4737	GAAAAGCAGTGAATTGAAATTCTGGCT--GTGAGTCACTCCAGAAACAAATTAC	4796	Db	312	TAAGCCCAGAGTCCAGGAGCACCAGAACATGTGATACAAACAGAAAGTGGATCTCTTCA	371
Qy	4820	GTTCCTATCATTAGACTGGATGCTGATGACAGCATTAAACAACTGTGAGCAGT	4879	Qy	2845	GCTTGGGAAATTATCTTCTTGGATGTTGCTGACGGCTTCAGAAAGGA	2904
Db	4797	GTTCCTATCATTAGACTGGATGCTGATGACAGCATTAAACAACTGTGAGCAGT	4856	Db	372	GCTTGGGAAATTATCTTCTTGGATGCTTCACTCCAGTGTGAGCTTCAAGAAAGGA	4311
Qy	4880	GCTGTAAGCCTGCCAAAGCAAGATACTCTAAATTAGTGTGTTGATGAAATTATAAC	4939	Qy	2905	TCTTGTGTCACAACTCAGAGATCCACCTTCGCTTCAAGTGTGAGCTTGTGAGC	2964
Db	4857	GCTGTAAGCCTGCCAAAGCAAGATACTCTAAATTAGTGTGTTGATGAAATTATAAC	4916	Db	432	TCTTGTGTCACAACTCAGAGATCCACCTTCGCTTCAAGTGTGAGCTTGTGAGC	491
Qy	4940	CAAAGTAGAAAAAAAGTGTGTCATTTCTGTACAGCTATAGATGACTACTAC	4999	Qy	2965	ATGGAAAGCATGCCAAGCAGAAATCTGTCATCTCTGGCTGTGAAACCGATCAGCAA	3024
Db	4917	CAAAGTAGAAAAAAAGTGTGTCATTTCTGTACAGCTATAGATGACTACTAC	4976	Db	492	ATGGAAAGCATGCCAAGCAGAAATCTGTCATCTCTGGCTGTGAAACCGATCAGCAA	551
Qy	5000	AATCTTATTTAA 5012		Qy	3025	AACGGCCCACGCCAAGAACTGTCAGAGTGGGTGCTGCCCAACCCAGATGGAGG	3084
Db	4977	AATCTTATTTAA 4989		Db	552	AACGGCCCACGCCAAGAACTGTCAGAGTGGGTGCTGCCCAACCCAGATGGAGG	611
Qy	3085	AGTCAGAGCTGTCATGAAGTGGTGCACACAGCTGACCAACAGTGGAAAGGCC		Qy	3145	GCACCATGATGCCGCAATGCTTCTCAGGGCATCTCCCTGCCATCGATTACAC	3144
Db	612	AGTCAGAGCTGTCATGAAGTGGTGCACACAGCTGACCAACAGTGGAAAGGCC		Db	672	GCACCATGATGCCGCAATGCTTCTCAGGGCATCTCCCTGCCATCGATTACAC	671
Qy	3145	GCACCATGATGCCGCAATGCTTCTCAGGGCATCTCCCTGCCATCGATTACAC		Qy	3205	ACAGCCACATGTCATGCCGCAATTTAAAGACATGGAGCTGTTCACTCC	3264
Db	672	GCACCATGATGCCGCAATGCTTCTCAGGGCATCTCCCTGCCATCGATTACAC		Db	732	ACAGCCACATGTCATGCCGCAATGCTTCTCAGGGCATCTCCCTGCCATCGATTACAC	731
Qy	3205	ACAGCCACATGTCATGCCGCAATTTAAAGACATGGAGCTGTTCACTCC		Qy	3265	GTGAAACCATGTCATGCCGCAATTTAAAGACATGGAGCTGTTCACTCC	3224
Db	792	GTGAAACCATGTCATGCCGCAATTTAAAGACATGGAGCTGTTCACTCC		Db	852	TGCTTCCGGAAACAGACAATAATATGAGCACAACTGCTCTATCATGGACACACA	851
Qy	3265	GTGAAACCATGTCATGCCGCAATTTAAAGACATGGAGCTGTTCACTCC		Qy	3325	TGCTTCCGGAAACAGACAATAATATGAGCACAACTGCTCTATCATGGACACACA	3384
Db	852	TGCTTCCGGAAACAGACAATAATATGAGCACAACTGCTCTATCATGGACACACA		Db	972	GAATAATAATTGATTTAAAGGATTAACGATAGAACTGTCATGAAAGTGGCTT	911
Qy	3325	TGCTTCCGGAAACAGACAATAATATGAGCACAACTGCTCTATCATGGACACACA		Qy	3385	GGGGATGCTGGTGTGTTGCTGAACTTCTGAGTTGATTTGTCACCTCTACCA	3444
Db	972	GAATAATAATTGATTTAAAGGATTAACGATAGAACTGTCATGAAAGTGGCTT		Db	912	GGGGATGCTGGTGTGTTGCTGAACTTCTGAGTTGATTTGTCACCTCTACCA	971
Qy	3385	GGGGATGCTGGTGTGTTGCTGAACTTCTGAGTTGATTTGTCACCTCTACCA		Qy	3445	GAATAATAATTGATTTAAAGGATTAACGATAGAACTGTCATGAAAGTGGCTT	3504
Db	912	GGGGATGCTGGTGTGTTGCTGAACTTCTGAGTTGATTTGTCACCTCTACCA		Db	972	GAATAATAATTGATTTAAAGGATTAACGATAGAACTGTCATGAAAGTGGCTT	1031
Qy	3445	GAATAATAATTGATTTAAAGGATTAACGATAGAACTGTCATGAAAGTGGCTT		Qy	3505	TAGATGATTTCATCCAAAGAACTTCTGAGTTGATTTGTCACCTCTACCA	3564
Db	972	GAATAATAATTGATTTAAAGGATTAACGATAGAACTGTCATGAAAGTGGCTT		Db	1032	TAGATGATTTCATCCAAAGAACTTCTGAGTTGATTTGTCACCTCTACCA	1091
Qy	3505	TAGATGATTTCATCCAAAGAACTTCTGAGTTGATTTGTCACCTCTACCA		Qy	3565	CCAAGACGCTTCTGCACTGCTGAAATTATCTACATCTGAAATTCTCAAGA	3624
Db	1032	TAGATGATTTCATCCAAAGAACTTCTGAGTTGATTTGTCACCTCTACCA		Db	1092	CCAAGACGCTTCTGCACTGCTGAAATTATCTACATCTGAAATTCTCAAGA	1151
Qy	3565	CCAAGACGCTTCTGCACTGCTGAAATTATCTACATCTGAAATTCTCAAGA		Qy	3625	TTCCCGCAGCTTCAAGAAAGAAATTACAGATTATTGACCATACATGGTATTGAA	3684
Db	1092	CCAAGACGCTTCTGCACTGCTGAAATTATCTACATCTGAAATTCTCAAGA		Db	1152	TTCCAGCAGCTTCAAGAAAGAAATTACAGATTATTGACCATACATGGTATTGAA	1211
Qy	3625	TTCCCGCAGCTTCAAGAAAGAAATTACAGATTATTGACCATACATGGTATTGAA		Db	1152	TTCCAGCAGCTTCAAGAAAGAAATTACAGATTATTGACCATACATGGTATTGAA	3744
Db	72	TTCCAGCAGCTTCAAGAAAGAAATTACAGATTATTGACCATACATGGTATTGAA		Qy	3685	CAATACTCTTACACTGTTGGAATCCAGAAAGATAAAACTCAGTCAGTCAAGTCA	

RESULT 3
 US-09-836-392-6
 ; Sequence 6, Application US/09836392
 ; Patent No. US20030173458A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptides, a
 ; FILE REFERENCE: PTO2001
 ; CURRENT APPLICATION NUMBER: US/09/8336,392
 ; PRIORITY APPLICATION NUMBER: 2001-04-18
 ; PRIORITY FILING DATE: 2000-10-11
 ; PRIORITY APPLICATION NUMBER: 60/159,542
 ; PRIORITY FILING DATE: 1999-10-15
 ; PRIORITY APPLICATION NUMBER: 60/165,914
 ; PRIORITY FILING DATE: 1999-11-17
 ; PRIORITY APPLICATION NUMBER: 60/189,027
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 2946
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-836-392-6

Query Match 53.0%; Score 2928.8; DB 9; Length 2946;
 Best Local Similarity 99.9%; Pred. No. 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2485 GCACTTAGAGACACCATGACAGGAGCTGATCGAGACCGTCAAGACTCTGGAGC 2544
 Db 12 GCACTTAGAGACACCATGACAGGAGCTGATCGAGACCGTCAAGACTCTGGAGC 71

Qy 2545 TTTCCTGAGAGATCTGGATGGATTAGTTATCCATGAGAAGGAAATGTTCAACGGG 2604
 Db 72 TTTCCTGAGAGATCTGGATGGATTAGTTATCCATGAGAAGGAAATGTTCAACGGG 131

1212	CAA TACT CCT TAC ACT GTG GGAT CCA AGGATA AA ACT CAAG TCA ATT TAAT TCT GT	1271	Db	2292	AAAGCAGTGC AAAT TGGAAATTCTGGCTGGGAACTACCAAAAGAAACATATTACAGTTT	2351
Qy			Qy	4825	TATCATTAAGAGTGGGATTCGTGATGAA CAGGCATTAAACACACTGTGAAAGCAGTGGTGT	4884
Db			Db	2352	TATCATTAAGGTGGATTCGTGATGAA CAGGCATTAAACACACTGTGAAAGCAGTGGTGT	2411
1242	ATGATGCTGTGACAGAGAAGCTGAGGGAGCTAACAGGAAAGTGGAAATTGTAAATTCTGT	3804	Qy	4885	CACGCTGC CAAAGCAAGATACTCTCAATTATTACTCTGTGAAATTAAACATCAAG	4944
Qy			Db	2412	CACCCCTGCCAAAGCAAGATACTCTCAATTATTACTCTGTGAAATTAAACATCAAG	2471
Db			Qy	4945	TAGAAAAGGGTGTCTGTGCTATTCTGTGCTATTCTGTGAAATTAAACATCAAG	5004
1272	ATGATGCTGTGAGAGGAGCTAACAGGAAAGTGGAAATTGTAAATTCTGT	1331	Qy	4945	TAGAAAAGGGTGTCTGTGCTATTCTGTGCTATTCTGTGAAATTAAACATCAAG	5004
Qy			Db	2472	TAGAAAAGGGTGTCTGTGCTATTCTGTGCTATTCTGTGAAATTAAACATCAAG	2531
Db			Qy	5005	TATTTAACCTTAAGAAACTGTGCTTAACCTCAATTACAGGGCTTAACTCGGA	5064
Qy			Db	2532	TATTTAACCTTAAGAAACTGTGCTTAACCTCAATTACAGGGCTTAACTCGGA	2591
Db			Qy	5065	ATAATGGAATGTGTTCTACATTCAATTAAATTCTAAAGAGGACTGTGCTGAA	5184
Qy			Db	2592	ATAATGGAATGTGTTCTACATTCAATTAAATTCTAAAGAGGACTGTGCTGAA	2651
Db			Qy	5125	CAGTCGCTCACACCTTAACTCCAGCACTTTAACTGGGAAAGCAGCAAGGAA	5184
Qy			Db	2652	CAGTCGCTCACACCTTAACTCCAGCACTTTAACTGGGAAAGCAGCAAGGAA	2711
Db			Qy	5185	ACCAAGGAGTTGAGACAGGCTTGGCAAAAGCCCATCTCTTAAACATCAA	5244
Qy			Db	2712	ACCAAGGAGTTGAGACAGGCTTGGCAAAAGCCCATCTCTTAAACATCAA	2771
Db			Qy	5245	AAAATTAGTGGGATGGNGCAATGGGCAATGGGCAATGGGCAATGGGCAATGGG	5304
Qy			Db	2772	AAAATTAGTGGGATGGGCAATGGGCAATGGGCAATGGGCAATGGGCAATGGG	2831
Db			Qy	5305	GATCATGTGAGCCPCTAGGAGTTGAGCTGTCAGTGTGACTGGCCACTGCATCC	5364
Qy			Db	2832	GATCATGTGAGCCPCTAGGAGTTGAGCTGTCAGTGTGACTGGCCACTGCATCC	2891
Db			Qy	5365	AGTCAGGGAAACAGAGCAAGACCTGTCTTAAAGGAAAGAAAAAAA	5416
Qy			Db	2892	AGTCAGGGAAACAGAGCAAGACCTGTCTTAAAGGAAAGAAAAAAA	2943
Db					RESULT 4	
					US - 09-925-301-184	
					Sequence 184, Application US /09925301	
					Patent No. US2002052308A1	
					GENERAL INFORMATION:	
					APPLICANT: Rosen et al.	
					FILE REFERENCE: PA106	
					CURRENT APPLICATION NUMBER: US /09-925, 301	
					PRIOR APPLICATION NUMBER: FCT /US00/05882	
					PRIOR FILING DATE: 2000-03-08	
					PRIOR APPLICATION NUMBER: 60/124, 270	
					PRIOR FILING DATE: 1999-03-12	
					NUMBER OF SEQ ID NOS: 1694	
					SOFTWARE: Patent in Ver...2.0	
					SEQ ID NO: 184	
					TYPE: DNA	
					ORGANISM: Homo sapiens	
					FEATURE:	
					NAME/KEY: misc feature	
					LOCATION: (2096)	
					OTHER INFORMATION: n equals a,t,g, or c	
					NAME/KEY: misc feature	
					LOCATION: (2140)	
					OTHER INFORMATION: n equals a,t,g, or c	
					NAME/KEY: misc feature	
					LOCATION: (2157)	
					OTHER INFORMATION: n equals a,t,g, or c	

;	NAME/KEY: misc feature	;	Db	909	TGAGGGAGATATGCCCTGGCTGATTGCCAGTTAAGGGCACANGCTCTGGGCAGT	968	
;	OTHER INFORMATION: n equals a,t,g, or c	;	Qy	4166	TCCCACTCCATTGGGTAGCATAGCTATGACAGATATCTGCTGCTCAGACAT	4225	
;	NAME/KEY: misc feature	;	Db	969	TCCCACTCCATTGGGTAGCATAGCTATGACAGATATCTGCTGCTCAGACAT	1028	
;	OTHER INFORMATION: n equals a,t,g, or c	;	Qy	4226	GGGAAATCTGTTACATAAGCTCTGTGACTCTCTGGTAAAGCTTGTCAAGATGTC	4285	
;	Best Local Similarity 38.0%; Score 2144.6; DB 10; Length 2200;	;	Db	1029	GGGAACTGTGATATAAGCTCTGTGACTCTCTGGTAAAGCTTGTCAAGATGTC	1088	
;	Matches 2173; Conservative 2; Mismatches 16; Indels 3; Gaps 2;	;	Qy	4286	TATGTCAGGGCATAACCTAACCCAGAACTCTGACCCAGGATCACAGCAAAAT	4345	
Db	69	TGAAACCATATCCGGATCTTTAAAGACATGGAGCTCAGTGTGACTCCACTACT	3265	Db	1089	TATGTCAGGGCATAACCTAACCCAGAAACTCTGACCCAGGATCACAGCAAAAT	1148
Qy	3266	TGAAACCATATCCGGATCTTTAAAGACATGGAGCTCAGTGTGACTCCACTACT	3325	Qy	4346	CATGTAAGACTCTGTCAGTCCAGGAACTCTGACCCAGGATCACAGCAAAAT	4405
Db	69	TGAAACCATATCCGGATCTTTAAAGACATGGAGCTCAGTGTGACTCCACTACT	128	Db	1149	CATGTAAGACTCTGTCAGTCCAGGAACTCTGACCCAGGATCACAGCAAAAT	1208
Qy	3326	GCTTCGGAAACAGAACAAATATAATGAGCAAAAGTGCCTTATCTGACCAAAAG	3385	Qy	4406	CACCTATGTGCCCTTGTCTGGATAAAGGGAGGCCATGTCAGGTTAAAGTGTGCA	4465
Db	129	GCTTCGGAAACAGAACAAATATAATGAGCAAAAGTGCCTTATCTGACCAAAAG	188	Db	1209	CACCTATGTGCCCTTGTCTGGATAAAGGGAGGCCATGTCAGGTTAAAGTGTGCA	1268
Qy	3386	CGGGATGCTGTTGATGCTCTTGTGACTCTGCGGATCCTTITGCAAGATAATG	3445	Qy	4466	GAAGGAAGGGAGACAGAGAACGGCTGTCAGGATGTGCAAACTCTGACCCATGTC	4525
Db	189	CGGGATGCTGTTGATGCTCTTGTGACTCTGCGGATCCTTITGCAAGATAATG	248	Db	1269	GAAGGAAGGGAGACAGAGAACGGCTGTCAGGATGTGCAAACTCTGACCCATGTC	1328
Qy	3446	AAATAATATATTGAAATTAAACGATACTGCTATGAAACCTGGTGTGCAAGG	3505	Qy	4526	GAAACTGAGGACTAAAGTCACTGATGAAAGAACTGAGGAACTTCCATAATTGTC	4585
Db	249	AAATAATATTTGAAATTAAACGATACTGCTATGAAACCTGGTGTGCAAGG	308	Db	1329	GAAACTGAGGACTAAAGTCACTGATGAAAGGAATGGAGGAACTTCCATAATTGTC	1388
Qy	3506	AGATCGATTTCATCCAAAGAACCTCTGGAGTGTGCAATTGTCACCTCTAAC	3565	Qy	4586	AGTGCATAATGTGAGGGCATTTCTCAATGCTTCAGGTTGAAATCCTGAGGC	4645
Db	309	AGATCGATTTCATCCAAAGAACCTCTGGAGTGTGCAATTGTCACCTCTAAC	368	Db	1389	AGTGCATAATGTGAGGGCATTTCTCAATGCTTCAGGTTGAAATCCTGAGGC	1448
Qy	3566	CAACNGCTTCTGCCCACTCTGGCAAACTTCTACACTCTATGAAATCATC	3625	Qy	4646	AACAGTGGTCCATTGTGAGGTGTCTAGGCCGGAAAGCTGTGCAAGCCAGCA	4705
Db	369	CAACNGCTTCTGCCCACTCTGGCAAACTTCTACACTCTATGAAATCATC	428	Db	1449	AACAGTGGTCCATTGTGAGGTGTCTAGGCCGGAAAGCTGTGCAAGCCAGCA	1508
Qy	3626	TCCAGCACTCAGGAAGAAATTCAGTATTATTGAACTCATGTTATTGAAAGC	3685	Qy	4706	GGCPTGAAACTCAGGTTAAACUCGACTTCAGCCTTGTGCAACTTACATCAGA	4765
Db	429	TCCAGCACTCAGGAAGAAATTCAGTATTGTGCAATTGTCACCTACATGTT	488	Db	1509	GGCPTGAAACTCAGGTTAAACUCGACTTCAGCCTTGTGCAACTTACATCAGA	1568
Qy	3686	AATACTCTACACTGTGGGATCCAGAAGATAAACTGCAAGTCACTTATTCTG	3745	Qy	4766	AAGCAGTGAATTTGAAATTGTCAGGCTTGTGGATCTGGTGTGGATCTGGT	4825
Db	489	AATACTCTACACTGTGGGATCCAGAAGATAAACTGCAAGTCACTTATTCTG	548	Db	1569	AAGCAGTGAATTTGAAATTCTGGTGTGGATCTGGTGTGGATCTGGT	1628
Qy	3746	TGATGCTGTCAGAGAAACCTGAGGAGAGTGTGAACTTGTAAATCTGTC	3805	Qy	4826	ATCATTAAGTGGATGCTGATGAAACAGGCAATTAAACACAACCTGTGCTG	4885
Db	549	TGATGCTGTCAGAGAAACCTGAGGAGAGTGTGAACTTGTAAATCTGTC	608	Db	1629	ATCATTAAGTGGATGCTGATGAAACAGGCAATTAAACACAACCTGTGCTG	1688
Qy	3806	TTCGCTCTTAATAGCTGTTGAGCTCTACAGTTATGCAAGGAGATTGCA	3865	Qy	4886	ACGCCCTGCCAAAGCAAGATACTCTTAACTTAACTTAACTTAACTCAAGT	4945
Db	609	TTCGCTCTTAATAGCTGTTGAGCTCTACAGTTATGCAAGGAGATTGCA	668	Db	1689	ACGCCCTGCCAAAGCAAGATACTCTTAACTTAACTTAACTCAAGT	1748
Qy	3866	AGATCTTATGCCAACAAATAAACTTCAATGTCAGCTCTACAGTTATGCA	3925	Qy	4946	AGAAAAAAAGGTGCTGCTGCTATTCTGTCAGCTTAACTTAACTCAAGT	5005
Db	669	AGATCTTATGCCAACAAATAAACTTCAATGTCAGCTCTACAGTTATGCA	728	Db	1749	AGAAAAAAAGGTGCTGCTGCTATTCTGTCAGCTTAACTTAACTCAAGT	1808
Qy	3926	GAAGTATGCTTAAAGAACCTGAGGAGGTGTGAAAGAAACCTGGCATCA	3985	Qy	5006	ATTTAACCTTAAGAACTGTCGTTAACTCAACAGAGGCTTAACTGGCAA	5065
Db	729	GAAGTATGCTTAAAGAACCTGAGGAGGTGTGAAAGAAACCTGGCATCA	788	Db	1809	ATTTAACCTTAAGAACTGTCGTTAACTCAACAGAGGCTTAACTGGCAA	1868
Qy	3986	GTTACAGGTTCTCATCAATTGGCTGGTTACAAACGGAAAGGCAATGGTAC	4045	Qy	5066	TAATGGAACTGTCAGCTTAACTCAAACTTAACTTAACTCAAGT	5125
Db	789	GTTACAGGTTCTCATCAATTGGCTGGTTACAAACGGAAAGGCAATGGTAC	848	Db	1869	TAATGGAACTGTCAGCTTAACTCAAACTTAACTTAACTCAAGT	1928
Qy	4046	CTTCAGGTTGTGGCTTACATCAAAACGGAAAGGCAACCTGGCTCGC	4105	Qy	5126	AGTGGCTCACACCCATTCACTGCTGCTGCTGCTGCTGCTGCTGCTG	5185
Db	819	CTTCAGGTTGTGGCTTACATCAAAACGGAAAGGCAACCTGGCTCGC	908	Db	1929	AGTGGCTCACACCCATTCACTGCTGCTGCTGCTGCTGCTGCTGCTG	1988
Qy	4106	TGGAGGAGATATGACCTGCTGATTCCCCAGTTAGGGCCACAGCTGGGCCAGT	4165	Qy	5186	CCAGGAGTTGAGACCACCTGGCAAAAGGAACCCATTCTCTATAAAACTAAA	5245

RESULT 6
US-09-918-995-24436
; Sequence 24416, Application US/09119995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-156
; CURRENT APPLICATION NUMBER: US/09-918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 24436
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(419)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-24436

Query Match 6.1%; Score 362.8; DB 9; Let
Best Local Similarity 95.6%; Pred. No. 5.5e-88;
Matches 373; Conservative 0; Mismatches 17; Inc

Query	Subject	Score	DB	Length
Qy	256 CTCGTGAGAACTATATGTAAGAGTCGATATTGAGGGTTAAATGGG	6.1%	9	419
Db	30 CGCTCGAGGAATTCGGAAATTCGGCAGGGTGGATTGAGGGTTATATGG			
Qy	316 ATCTAGTTCCTGAAATAATAGACTTAAAAATGCAAAAGGTCTATCA			
Db	90 ATCTAGTTCCTGAAATAATAGAGTTAAAATGCAAAAGGTCTATCA			
Qy	316 TGTAAATCTCGCTAGAAGACTGCCAGAAGCTCGCCAAAGAAACACTGTGG			
Db	150 TGTAAATCTCGCTAGAAGAACTGCCAAAGAAACACTGTGG			
Qy	436 AACCTGGCTTACCACTGGAGTCAATTCTAGGGAGCTAAACAA			
Db	210 AACCTGGCTTACCACTGGAGTCAATTCTAGGGAGCTAAACAA			
Qy	496 TTCTATGAAAGAAATGCTGAAAGCCGGCTCAGGGAGGACCAA			
Db	270 TTCTATGAAAGAAATGCTGAAAGCCGGCTCAGGGAGGACCAA			
Qy	556 AGCGGAAAGAAAGCCGGAGGAAACCTGAAATTCTGATGAGAT			
Db	330 AGCGGAAAGAAAGCCGGAGGAAACCTGAAATTCTGATGAGAT			
Qy	616 AGATAAAAGAAAGGAAAAAGGAAACAA	6.15	9	419
Db	390 AGATAAAAGAAAGGAAAAAGGAAACAA			

RESULT 7
US-10-060-036-1707/C
; Sequence 1707, Application US/10060036
; GENERAL INFORMATION:
; APPLICANT: Benios, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.

APPLICANT: Jiang, yugu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
OF PANCREATIC CANCER
FILE REFERENCE: 210121_566
CURRENT APPLICATION NUMBER: US/10/060, 036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1707
LENGTH: 251
TYPE: DNA
ORGANISM: *Homo sapiens*
FEATURE:
NAME/KEY: misc_feature
LOCATION: 244
OTHER INFORMATION: n = A, T, C or G

Query	Match	Score	Length	DB	9;
Best	Local	Similarity	4.5%		
Matches	249	Conservative	99.2%	Pred. No.	4..6-57;
			0;	Mismatches	0;
				Indels	0;
2y					
4724	ACAAACTCGACTTGAGACCTCCCTGCCAACTACATCGAAAGACTGAA				
2y					
251	ACAAACTINGACTCGAGCCCTCTGCCAACTACATCGAAAGACTGAA				
2y					
4784	TCTGGCTGTGATATTCTACCCAAAGAACAAATTACAGTTTACATTAGAT				
2y					
191	TCTGGCTGTGATCTACCGAAAGAACAAATTACAGTTTACATTAGAT				
2y					
4844	TGATGACAGGCAATTAAACACAACTGTGAGCACTGTGCTGCTGCGCAA				
2y					
131	TGATGACAGGCAATTAAACACAACTGTGAGCACTGTGCTGCTGCGCAA				
2y					
4904	ATACCTCAAATTACTCTGTGATCAAATTATAACATCAAGTGAAGAAAGG				
2y					
71	ATACCTCAAATTACTCTGTGATCAAATTATAACATCAAGTGAAGAAAGG				
2y					
4964	GCTTATTCTGT	4.974			
2y					
11	GCTTATTCTGT	1			
2y					

RESULT 8
US-09-764-877-3220/c1
Sequence 3220, Application US/09764877
Patent No. US002014714A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09-764-877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 3220

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QY 5234 TAAAAACTAAAAATTAGTTGGCATGGGACATGGCTGTAGTCCTCCAGCTACTCAG 5293
Db 18234 CAAAAATACAAAATTAGCTGGCTTGGCTTAACTCCAGCTACTCAGG 18175
QY 5294 AGGTGAGT- -GGATCATCTGAGCTAGGTTGAGGCTGAGCTGTGACT 5349
Db 18174 AGGTGAGTGGTAGGAGTACCTGTAGCTGGGAGGTAGGGTCAAGGCTGAGCTGAGGAA 18115
QY 5350 GGCCTACTGGACTCCAGCTGGACAAACAGAGAGACCCGTCTTAAAAAAAGAA 5409
Db 18114 GCACACCTCAGCTCAGCTGGG-CAGAGAGACCCGTGTAANAAAAGA 18056
QY 5410 AAAAAAA 5416
Db 18055 AAAGAAA 18049

RESULT 9
US-09-742-312-3
; Sequence 3, Application US/09742312
; Patent No. US2009015166A1
; GENERAL INFORMATION:
; APPLICANT: CHANDRAMOLISARAN, Ishwar er al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEIN
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO000838
; CURRENT APPLICATION NUMBER: US/09/742,312
; CURRENT FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: fastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 147309
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; LOCATION: (1)-(147309)
; OTHER INFORMATION: n = A, T, C or G
; FWD 00 742 312-3

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SEQ ID NO 3
 LENGTH: 326014
 TYPE: DNA
 ORGANISM: Human
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(326014)
 OTHER INFORMATION: n = A, T, C or G
 US-09-731-23A-3

Query Match Score 188.2; DB 10; Length 326014;
 Best Local Similarity 77.8%; Prc. No. 2e-38;
 Matches 253; Conservative 0; Mismatches 68; Indels 4; Gaps 2;

QY	5101	TAATTCTAAGAAGGGCTGGTCACTGGCTAACACCTTAATCCAGGACTTGGAA	5160
DB	36647	TAAGGCTCATTGGTAGATGGTAGCTAACACTGTAATCTAGACTTGTGAG	36588
QY	5161	GCCAGGGAGGAGAGCTGTTGAAACCCGGAGTTGAGACCCCTGAGCAACAAAGCAA	5220
DB	36587	GCCAGGGAGAATGCTTAAGTCCAGGGAGCTTCAAGCCGCTGGGACATAGTGA	36528
QY	5221	GACCCATCTCTATAAAACTAAAAATTAGTTGGCATGGGCACATGCCCTGAGTC	5280
DB	36527	GACCCCTCTCTATAAAAGTAAAAATTAGCTGGCATGGCTGAGTC	36468
QY	5281	CCAGCTATCCAGGGCTGAGATGGTATCTG--AGCCTAGGGTGGAGGTGAG	5337
DB	36467	CCAGCTACTTGGAGGTGGAGACTGCTCTGGCTAACCCCTAGGGTGGAGTC	36408
QY	5338	TGAGCTGTGACTCGCCACTGCAGTCTGGACAGAGCAAGACCTGCTTAA	5397
DB	36407	TGAGCTGTGACTCGCCACTGCAGTCTGGCTAACCCCTAGGGTGGAGTC	36349
QY	5398	AAAAAAAAAGAAAAAAATTTTTT	5422
DB	36348	AAAAATAACAAAATAATATTATTTTT	36324

RESULT 13
 US-09-842-364-1/C
 Sequence 1, Application US/09842364
 GENERAL INFORMATION
 APPLICANT: Yen Potin, Frances
 APPLICANT: Denison, Blake
 APPLICANT: Bour, Barbara
 APPLICANT: Bihain, Bernard
 APPLICANT: Dumas Mine Edwards, Jean-Baptiste
 APPLICANT: Duclerc, Aymeric
 APPLICANT: Bougueret, Lydie
 TITLE OF INVENTION: APOLIPOPROTEIN A-IV-RELATED PROTEIN: POLYPEPTIDE, POLYNUCLEOTIDE
 TITLE OF INVENTION: SEQUENCES AND BIALLELIC MARKERS THEREOF.
 FILE REFERENCE: GENSET 50CP/C
 CURRENT FILING DATE: 2001-04-25
 PRIOR APPLICATION NUMBER: US/09/842/364
 PRIOR FILING DATE: 2000-06-21
 PRIOR APPLICATION NUMBER: PCT/IB99/02058
 PRIOR FILING DATE: 1999-12-20
 PRIOR APPLICATION NUMBER: US 09/469/099
 PRIOR FILING DATE: 1999-12-21
 PRIOR APPLICATION NUMBER: US 60/113,686
 PRIOR FILING DATE: 1998-12-22
 PRIOR APPLICATION NUMBER: US 60/141,032
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: Patent-pm

SEQ ID NO 1
 LENGTH: 81001
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE: primer_bind

LOCATION: 1220..1238
OTHER INFORMATION: 20-828-311.mis
NAME/KEY: primer_bind

LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement
NAME/KEY: primer_bind

LOCATION: 1232..12346
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer_bind

LOCATION: 12348..12366
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer_bind

LOCATION: 1522..15240
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind

LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer_bind

LOCATION: 4219..42217
OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer_bind

LOCATION: 42219..42237
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer_bind

LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer_bind

LOCATION: 55443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer_bind

LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer_bind

LOCATION: 1227..1251
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc_binding

LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc_binding

LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc_binding

LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc_binding

LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc_binding

LOCATION: 77046..77070
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc_binding

US-09-842-364-1

Query Match 3..4%; Score 187..6; DB 9; Length 81001;
Best Local Similarity 71.1%; Pred. No. 1e-38; 3; Gaps 1;
Matches 263; Conservative

Qy 5054 TCTCATATTAAATTCTAAGAAGGGCTGCTACACCTTAA 5143
Db 65068 TTACCCCTGATTACAAATAGGAATTGTGGCCAGGGTACGGCTGTAA 65009

Qy 5114 TCCAGGCATTTGGAAAGCCAGGCAAGAAGACTGCTGAAACCGGAGCAG 5203
Db 65008 TCCAGGCATTTGGAGCAGGGTGGTGTACCTGGTGGATGAGGTTGAGACCG 64949

Qy 5204 CCTGAGCAAAAGCAAGAACCCATCTCTAAAAACTAAATAATTAGTGGGATGT 5223

Db 64948 CCTGGCCAACATGTGAAACCCGGTCATTAATAATTAGGGGATGT 64889

Qy 5264 GGCACATGCTGTAGTCCAGTACTCCAGGCTAG--ATGGATCATCTGAGCCCTA 5320

Db 64888 GGCGAGGGCCCTTAATCCAGCTACTAGGAGCTAGGGCAGGAAATCACTTGACCCG 64829
Qy 5321 GGAGGTTGAGGTGCACTGAGCTGACTGGCCACTGCACCTCCACTGCAGCTGGGACACAGA 5380
Db 64828 GGAGGCGAGGTGCACTGAGCTGACTGGCCACTGCACCTCCACTGCAGCTGGGACACAGA 64769
Qy 5381 GCAAGACCCCTGCTTAAGAAAAAAATTTCTAAGAAGGCTGCTCTA 5440
Db 64768 GCGAGACTCTGTATCAAAAAAAACAAAAAAATAATAAGGAAACTGTGGCTCAG 64709

Db 64708 AGAGATTAAG 64699

RESULT 14
US-09-751-877-1/c
; Sequence 1, Application US/09751877
; Patent No. US20020142942A1
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara
; APPLICANT: Bihain, Bernard
; APPLICANT: Dumas, Milne Edwards, Jean-Baptiste
; APPLICANT: Ducleir, Aymeric
; APPLICANT: Bouquellet, Lydie
; APPLICANT: Ebets- Reed, Diana
; APPLICANT: Salter-Cid, Luisa
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
; CURRENT APPLICATION NUMBER: US/09-751,877
; CURRENT FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 1
; LENGTH: 81001
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10946..12946
; OTHER INFORMATION: 5-regulatory region
; NAME/KEY: exon
; LOCATION: 12947..12958
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 13470..13526
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: 13641..13752
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
; LOCATION: 14271..15968
; OTHER INFORMATION: exon 4
; NAME/KEY: misc_feature
; LOCATION: 15369..17969
; OTHER INFORMATION: 3-regulatory region
; NAME/KEY: allele
; LOCATION: 12.9
; OTHER INFORMATION: 20-828-311 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 12.47
; OTHER INFORMATION: 17-42-31.9 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 15241
; OTHER INFORMATION: 17-41-250 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 42218
; OTHER INFORMATION: 20-841-149 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 45442
; OTHER INFORMATION: 20-842-115 : polymorphic base A or G

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NAME/KEY: allele
LOCATION: 77058
OTHER INFORMATION: 20-853-415 : polymorphic base C or T
NAME/KEY: primer_bind
LOCATION: 929_979
OTHER INFORMATION: 20-828.pu
NAME/KEY: primer_bind
LOCATION: 1357_1377
OTHER INFORMATION: 20-828_rp complement
NAME/KEY: primer_bind
LOCATION: 12029_12050
OTHER INFORMATION: 17-42.pu
NAME/KEY: primer_bind
LOCATION: 12581_12603
OTHER INFORMATION: 17-42_rp complement
NAME/KEY: primer_bind
LOCATION: 14992_15012
OTHER INFORMATION: 17-41.pu
NAME/KEY: primer_bind
LOCATION: 15460_15482
OTHER INFORMATION: 17-41_rp complement
NAME/KEY: primer_bind
LOCATION: 42070_42090
OTHER INFORMATION: 20-841.pu
NAME/KEY: primer_bind
LOCATION: 42572_42591
OTHER INFORMATION: 20-841_rp complement
NAME/KEY: primer_bind
LOCATION: 45328_45347
OTHER INFORMATION: 20-842.pu
NAME/KEY: primer_bind
LOCATION: 45863_45883
OTHER INFORMATION: 20-842_rp complement
NAME/KEY: primer_bind
LOCATION: 7664_76664
OTHER INFORMATION: 20-853.pu
NAME/KEY: primer_bind
LOCATION: 77166_77185
OTHER INFORMATION: 20-853_rp complement
NAME/KEY: primer_bind
LOCATION: 1220_1238
OTHER INFORMATION: 20-828-311.mis
NAME/KEY: primer_bind
LOCATION: 1240_1258
OTHER INFORMATION: 20-828-311.mis complement
NAME/KEY: primer_bind
LOCATION: 12328_12346
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer_bind
LOCATION: 12348_12366
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer_bind
LOCATION: 15222_15240
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind
LOCATION: 15242_15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer_bind
LOCATION: 42199_42217
OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer_bind
LOCATION: 42219_42237
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer_bind
LOCATION: 45423_45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 45443_45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer_bind
LOCATION: 77039_77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer_bind
; LOCATION: 77059..77077
; OTHER INFORMATION: 20-853-415.mis complement
; NAME/KEY: misc_binding
; LOCATION: 1227..1251
; OTHER INFORMATION: 20-828-311.probe
; NAME/KEY: misc_binding
; LOCATION: 12335..12359
; OTHER INFORMATION: 17-42-319.probe
; NAME/KEY: misc_binding
; LOCATION: 15229..15253
; OTHER INFORMATION: 17-41-250.probe
; NAME/KEY: misc_binding
; LOCATION: 2206..42230
; OTHER INFORMATION: 20-841-149.probe
; NAME/KEY: misc_binding
; LOCATION: 45430..45454
; OTHER INFORMATION: 20-842-115.probe
; NAME/KEY: misc_binding
; LOCATION: 77046..77070
; OTHER INFORMATION: 20-853-415.probe
US-09-751-877-1

Query Match Score 187.6; DB 10; Length 81001;
Best Local Similarity 71.1%; Pred. No. 1e-38;
Matches 263; Conservative 0; Mismatches 104; Indels 3; Gaps 1;
Qy 5084 TCATCATPAAATTAAATTAAATTCTAGAGAAGGGCTGGCTGAGGGCTCACACCTTAA 5143
Db 65068 TIAACCCTGATTTACAAATAGGAATTTGTGTGTGGCAAGGTCAGTCAGCTGCTGTAA 65009
Qy 5144 TCCCAGGACTTGTGGAGGCCAAGGGCAGGAAACTGCTTGAACCCAGAGTTGAGACAG 5203
Db 65008 TCCCAAGACTTGGGGCAAGGTTGGGTGATCACCTGAGGTGAGTCAGTTGAGTCACRG 64949
Qy 5204 CCTGAGGAAACAAGGAAGACCCATCTCTATAAAACTAAAAAATTAGTGGCTATGGT 5263
Db 64948 CCTGGCCAAACATGGTAAACCCCGTCTCTATTAAATAACAAATAGCGGGATGGT 64889
Qy 5264 GGCACATGCCCTGATGTCCAGCTACTCCAGGTGACTCAGGCTGAG -- ATGGATCATCTGAGCTCA 5320
Db 64888 GGCAGGAGGCCCTGTAATCCAGCTACTCAGGCTGAGGAAATCATTGAAACCCG 64829
Qy 5321 GGAGGTGAGGTGAGCTGCACTGCTGAGCTGCCACTCCAGTCTGGACAAACAGA 5380
Db 64828 GGAGGGGAGGTGAGCTGAGCTGCCACTCCAGTCTGGACAAACAGA 64769
Qy 5381 GCAAGGCCCTGTCATAAAGAAAAAAATTTTTCTAAAGACTGCTCCPA 5440
Db 64768 GCGAGACTCTGTCTATCAAAACAAACAAACAAATAAATAGGAAACTGTGGCTCAG 64709
Qy 5441 CAAAGTGTGAG 5450
Db 64708 AGAAAGTTAAG 64699

RESULT 15
US-09-764-872-812/c
; Sequence 812, Application US/09764872
; Publication No. US20030050231A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA125
; CURRENT APPLICATION NUMBER: US/09764-872
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 957
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 812
; LENGTH: 31718
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-872-812

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Query Match Score 187 4; DB 9; Length 31718;
 Best Local Similarity 75.4%; Pred. No. 5.9e-39;
 Matches 260; Conservative 0; Mismatches 81; Indels 4; Gaps 2;
 Matches 260; Conservative 0; Mismatches 81; Indels 4; Gaps 2;

Qy 5097 AAATTAAATCTAAAGAAGGGTGGTGTGCACTGGCTCACCTTAATCCAGGACTTGTG 5156
 Db 3273 AAGAGAACGCTCTCAGACGGGGTGGCTCACCTGTAAATCCAGGACTTGTG 3214

Qy 5157 GGAAGCCAGGGAGAACCTGAAACCCAGGACTTGTAGACCTGCTGAGAACACAA 5216
 Db 3213 GGGGCCAGGCAAGGCGGATCACCTGAGGTGAGGTTGAGCTGGGCGACATG 3154

Qy 5217 GCGAGACCCATCTCTATAAAACTAAAAAAATTAGTTGGCATGTCGACATGCCCTGT 5276
 Db 3153 GCGAAACCCATCTCTAAATAAGAAATTAGTAGCTGACATGGGACATGCCCTGT 3034

Qy 5277 AGTCCAGGCTACTCAGAGCTGAG--ATTGATCATCTGAGCTCAGGGGTGAGGT 5333
 Db 3093 AAGCCCGCTACTTGGAGGTGAGGCTAAAGAATCCCTTGAAACCCAGGCAAGGGT 3034

Qy 5334 GCAGTGAGGTGACTGGCACTGGCACTGGCTCGGACACAGAACGAGACCTGTC 5333
 Db 3033 GCAGTGAGGTGAGACTGGCACTGGCCACTGGACTCCAGCTGGG-CAAAGAAAAGACTCTGTC 2975

Qy 5394 TTAAAAAAAAGAAAAAAATTTTCTAAGAGCTGTCC 5438
 Db 2974 TCAGAAAAAAAGAACATGCTCTATTCAAGGTGTC 2930

Search completed: June 12, 2003, 04:54:41
 Job time : 710 secs